NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBd01D08

Lot# : 7677_B4Gp

Vector : pGCAP10

Gene	TCEB3	
RefSeq_mRNA	NM_003198.3	4838 bp

● Plasmid DNA purification

Date : 2024/07/25 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2024/07/26 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2024/07/26

DNA concentration (O.D.): 84 ng/ul

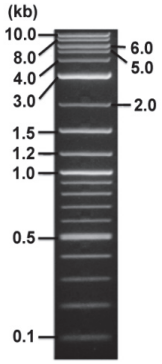
DNA	1.2 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	6.8 ul
Total	10 ul

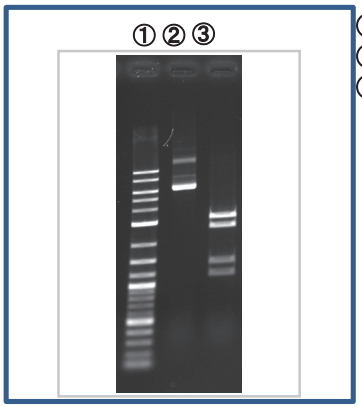
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.6, 1.3, 1.1 kb

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

Marker : 2-Log DNA Ladder (NEB#N3200L)





①:Marker
②:uncut
③:BamHI

● Confirmation of the insertion sequence

Date : 2024/07/30

Primer A	-
Primer B	-
Primer C	RBd01D08hts.seq
List of Sequencing Primers	-

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2024/07/31

DNA (84 ng/ul)	82 ul
10x TE	28 ul
dH_2O	166 ul
Total	276 ul

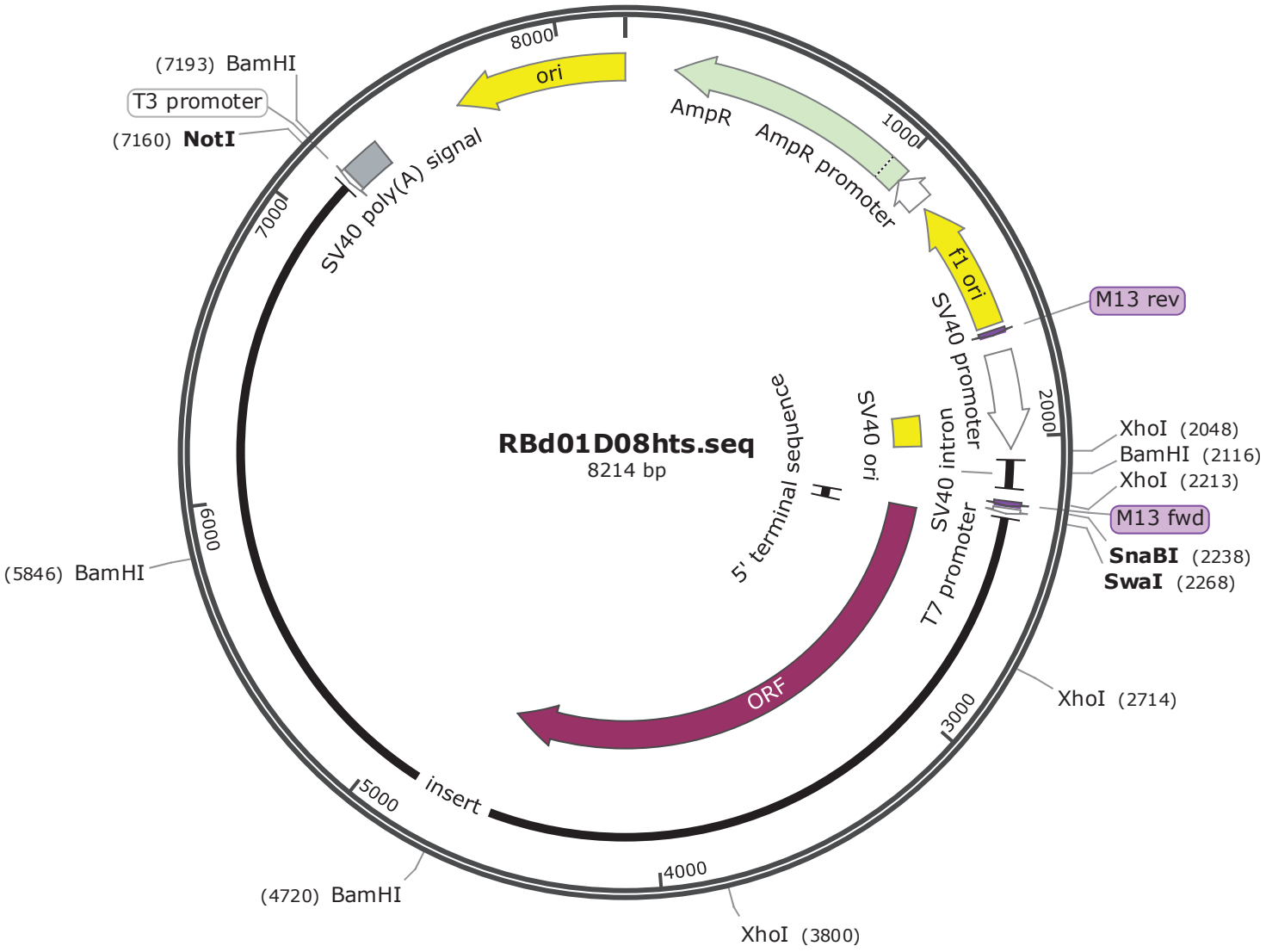
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '24.07.31 笹沼

http://dna.brc.riken.jp/index.html


RBd01D08hts.seq
8214 bp
8000
1000
2000
3000
4000
5000
6000
7000
ori
AmpR
AmpR promoter
f1 ori
SV40 promoter
SV40 intron
T7 promoter
SV40 ori
5' terminal sequence
ORF
insert
SV40 poly(A) signal
T3 promoter
(7193) BamHI
(7160) NotI
M13 rev
XhoI (2048)
BamHI (2116)
XhoI (2213)
M13 fwd
SnaBI (2238)
SwaI (2268)
XhoI (2714)
XhoI (3800)
(4720) BamHI
(5846) BamHI

BLAST Results

Questions/comments

Blast 2 sequences

Job title: ref|NM_003198.3|

RID AGEEDWN6114 (Expires on 07-31 08:54 am)

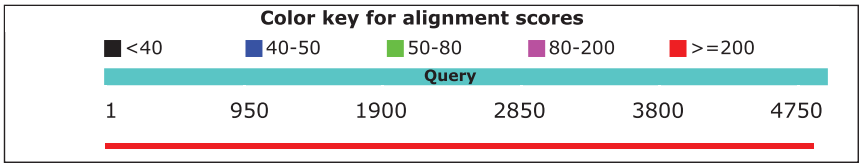
Query ID NM_003198.3
Description Homo sapiens elongin A (ELOA), mRNA
Molecule type nucleic acid
Query Length 4838

Subject ID lcl|Query_5053459
Description None
See details
Molecule type dna
Subject Length 8214
Program BLASTN 2.16.0+

RBd01D08hts.seq

Graphic Summary

Distribution of the top 1 Blast Hits on 1 subject sequences



Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	8909	8909	99%	0.0	99.98%	Query_5053459

Alignments

Sequence ID: Query_5053459 Length: 8214 Number of Matches: 1
Range 1: 2278 to 7104

Score	Expect	Identities	Gaps	Strand	Frame
8909 bits(4824)	0.0()	4826/4827(99%)	0/4827(0%)	Plus/Plus	

Features:

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CDS:elongin-A [Homo   1                       M  A  A  E  S  A  L  Q  V  V  E  K  L
Query                 12    GGAGGCCGCGCCAGTGACAGCGATGGCGGCGGAGTCGGCGCTCCAAGTTGTGGAGAAGCT  71
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 2278  GGAGGCCGCGCCAGTGACAGCGATGGCGGCGGAGTCGGCGCTCCAAGTTGTGGAGAAGCT  2337

CDS:elongin-A [Homo   14      Q  A  R  L  A  A  N  P  D  P  K  K  L  L  K  Y  L  K  K  L
Query                 72    GCAGGCGCGCCTGGCCGCGAACCCGGACCCTAAGAAGCTATTGAAATATTTGAAGAAACT  131
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 2338  GCAGGCGCGCCTGGCCGCGAACCCGGACCCTAAGAAGCTATTGAAATATTTGAAGAAACT  2397

CDS:elongin-A [Homo   34      S  T  L  P  I  T  V  D  I  L  A  E  T  G  V  G  K  T  V  N
Query                 132   CTCCACCCTGCCTATTACAGTAGACATTCTTGCGGAGACTGGGGTTGGGAAAACAGTAAA  191
                            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                 2398  CTCCACCCTGCCTATTACAGTAGACATTCTTGCGGAGACTGGGGTTGGGAAAACAGTAAA  2457

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Sbjct                 2458  TAGCTTGCGAAAACACGAGCATGTTGGAAGCTTTGCCAGGGACCTAGTGGCCCAGTGGAA  2517

CDS:elongin-A [Homo   74      K  L  V  P  V  E  R  N  A  E  P  D  E  Q  D  F  E  K  S  N
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Sbjct                2518  GAAGCTGGTTCCTGTGGAACGAAATGCTGAGCCTGATGAACAGGACTTTGAGAAGAGCAA  2577

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Sbjct                2578  TTCCCGAAAGCGCCCTCGGGATGCCCTGCAGAAGGAGGAGGAGATGGAGGGGGACTACCA  2637

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Sbjct                2638  AGAAACCTGGAAAGCCACGGGGAGCCGATCCTATAGCCCTGACCACAGGCAGAAGAAACA  2697

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Query                432  TAGGAAACTCTCGGAGCTCGAGAGACCTCACAAAGTGTCTCACGGTCATGAGAGGAGAGA  491
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Sbjct                2698  TAGGAAACTCTCGGAGCTCGAGAGACCTCACAAAGTGTCTCACGGTCATGAGAGGAGAGA  2757

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Query                612  CTACAGATCCCTGGAGGAGGACCAGGAGCCCATTGTTTCACACCAGAAGCCTGGGAAAGG  671
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Query                672  CCACAGCAATGCCTTTCAGGACAGACTCGGGGCCAGCCAAGAACGACACCTGGGTGAACC  731
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Sbjct                2938  CCACAGCAATGCCTTTCAGGACAGACTCGGGGCCAGCCAAGAACGACACCTGGGTGAACC  2997

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Query                732  CCATGGGAAAGGGGTTGTGAGTCAAAACAAGGAGCACAAATCTTCCCACAAGGACAAACG  791
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Sbjct                3118  GGCCCTCTCCAAAGAGGAGAACCGAAGGCCACCCTCAGGGGACAATGCAAGGGAGAAACC  3177

CDS:elongin-A [Homo   294    P  S  S  G  V  K  K  E  K  D  R  E  G  S  S  L  K  K  K  C
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Sbjct                3358  AGCAGGAGACCTGTTGCCCAAGGTAAAAGAGAAGGGTTCTAACAACCTAAAGACTCCAGA  3417

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Sbjct                3418  AGGGAAAGTCAAAACTAATTTGGATAGAAAGTCACTGGGCTCCCTCCCTAAAGTTGAGGA  3477

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Query               1272  TGACCAGCCCCGGAAGAAAAAGAAAAAGATTGTGAAAACTTCAGCCACGGCACTTGGAGA  1331
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CDS:elongin-A [Homo   634    Q  D  A  R  E  Q  R  L  R  V  L  T  K  N  I  Q  F  A  H  A
Query                1932  TCAGGACGCCCGAGAGCAGCGGCTACGAGTACTAACAAAGAATATCCAGTTCGCACATGC  1991
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CDS:elongin-A [Homo   654    N  K  P  K  G  R  Q  A  K  M  A  F  V  N  S  V  A  K  P  P
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Sbjct                4318  TCGTGACGTCCGGAGGAGGCAGGAAAAGTTTGGAACGGGAGGAGCAGCTGTCCCTGAGAA  4377

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Query                2112  AATCAAGATCAAGCCAGCCCCGTACCCCATGGGAAGCAGCCATGCTTCCGCCAGTAGCAT  2171
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Sbjct                4378  AATCAAGATCAAGCCAGCCCCGTACCCCATGGGAAGCAGCCATGCTTCCGCCAGTAGCAT  4437

CDS:elongin-A [Homo   714    S  F  N  P  S  P  E  E  P  A  Y  D  G  P  S  T  S  S  A  H
Query                2172  CAGCTTTAACCCCAGCCCTGAGGAGCCGGCCTATGATGGCCCAAGCACCAGCAGTGCCCA  2231
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4438  CAGCTTTAACCCCAGCCCTGAGGAGCCGGCCTATGATGGCCCAAGCACCAGCAGTGCCCA  4497

CDS:elongin-A [Homo   734    L  A  P  V  V  S  S  T  V  S  Y  D  P  R  K  P  T  V  K  K
Query                2232  CTTGGCACCAGTGGTCAGCAGCACTGTTTCCTATGATCCTAGGAAACCCACTGTGAAGAA  2291
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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CDS:elongin-A [Homo   754    I  A  P  M  M  A  K  T  I  K  A  F  K  N  R  F  S  R  R
Query                2292  AATTGCCCCAATGATGGCCAAGACAATTAAAGCTTTCAAGAACAGATTCTCCCGACGATA  2351
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Query                2352  AACTGAGGACTTGCCTTGGAAATGGAATCTGGGGAGGCAGGAATACAAGGACAGTGGGGG  2411
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Sbjct                4618  AACTGAGGACTTGCCTTGGAAATGGAATCTGGGGAGGCAGGAATACAAGGACAGTGGGGG  4677

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                           ..............................................................

                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4678  TTGGGGAATGGAATTCTACAGGAGACTGGAGTCTTGCTTTGTGGATCCTTTTGGTCTCCG  4737

Query                2472  AGTCCTGCAGTCTGCAGGTGCTGCCCCTGGGAACCTGCGTGCCACAGCCCCGCCTCCCTG  2531
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                4738  AGTCCTGCAGTCTGCAGGTGCTGCCCCTGGGAACCTGCGTGCCACAGCCCCGCCTCCCTG  4797

Query                2532  CCTGGAGCACACTTTAGAATTCTGAAGATGTGAAGCCTCTGTCTCACTGAGGATTTTAAA  2591
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct                4858  GGTCAATTATACTTTTGTTGTTCATTAGCATCTTTGTAAACTATAAGACGTAGTTTTAAT  4917

Query                2652  TAATAAATATTGCCCCCAGATTGTATTTATATTATCCCCCAGGtttgtttttgttttttG  2711
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Sbjct                4918  TAATAAATATTGCCCCCAGATTGTATTTATATTATCCCCCAGGTTTGTTTTTGTTTTTTG  4977

Query                2712  TCCTCTACCACACATTTAGCCTTTTATCTTCCAGGTCCTTATTAAAATCAGATGAAAGCC  2771
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Query                2772  TAGTGAAAGCCAGTCTCCTGCCCCAGCTCAGCTCTGTGTGGACTCTGGTCCAGACAGAGG  2831
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Query                2832  ACTGGGCATCTCCAGAGCCTGCACAGTACCTGCTGCACGTAGGGCAAGGAATGAGCACTA  2891
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Query                2892  GACCGCCTGTCCCCAAGGGAGCCTCAGTGGGGCGACAGGGTGCTCGGCGGACTCCACCTC  2951
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Sbjct                5158  GACCGCCTGTCCCCAAGGGAGCCTCAGTGGGGCGACAGGGTGCTCGGCGGACTCCACCTC  5217

Query                2952  AGGCCCTCCCCACTGTTGCTGTGCATTCCTGTGCAGGTGCATCTCTTTCTTACTAACTGG  3011
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Sbjct                5218  AGGCCCTCCCCACTGTTGCTGTGCATTCCTGTGCAGGTGCATCTCTTTCTTACTAACTGG  5277

Query                3012  TATTTATTAAGGGAGGTGCTCTGTAGGTCTGGAGCCTTTCCCTCATCCTTTTTGCGAGTC  3071
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Sbjct                5278  TATTTATTAAGGGAGGTGCTCTGTAGGTCTGGAGCCTTTCCCTCATCCTTTTTGCGAGTC  5337

Query                3072  CCCACCttttttgttttttttttttttCTTTGAGGCTCACTAGAGGACGCAGAACCTTGGGA  3131
                           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct                5338  CCCACCTTTTTGTTTTTTTTTTTTTCTTTGAGGCTCACTAGAGGACGCAGAACCTTGGGA  5397

Query                3132  GATTGATTTGCACAGAACTCCCCACCTCCCACTTTTACAATTTCCAGTTTCTGATTGAAA  3191
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Query                3192  ATTTTAGGGTTTCTCCCCACTGCCCTTCCCTATCTTTCCTTCCCCTCAACACCATGAAGG  3251
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